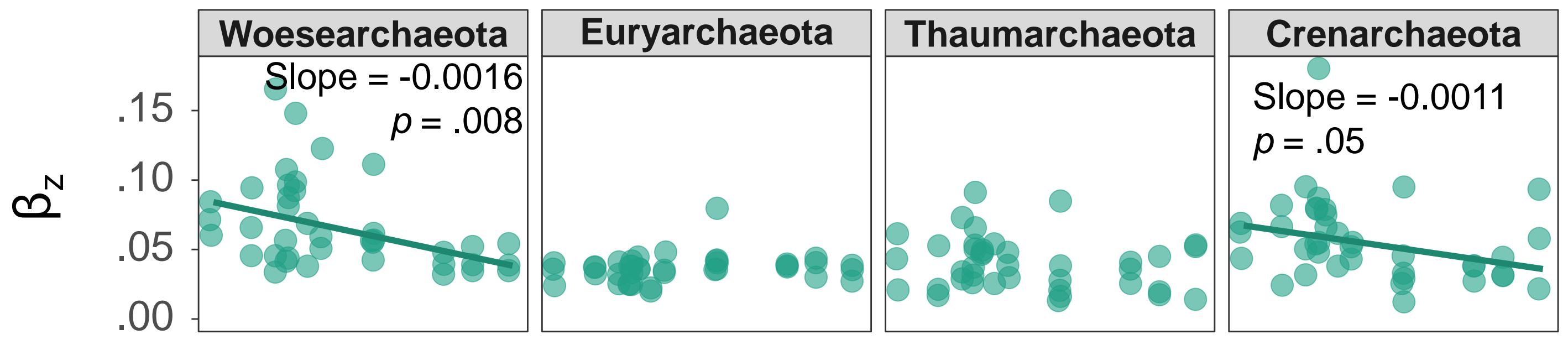
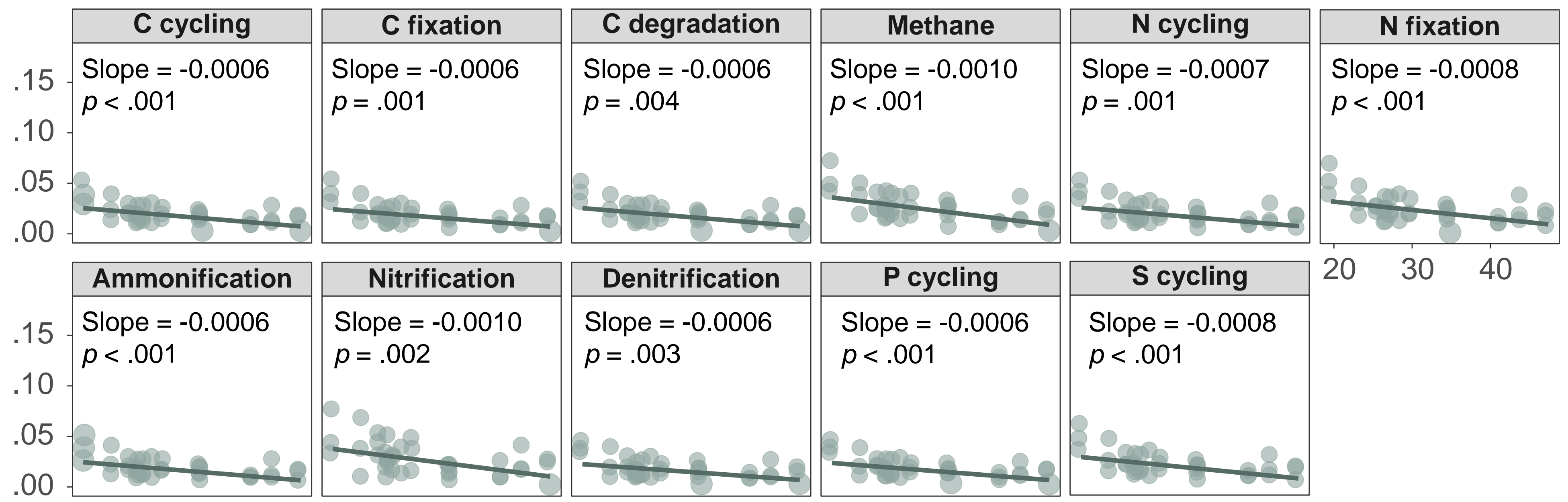
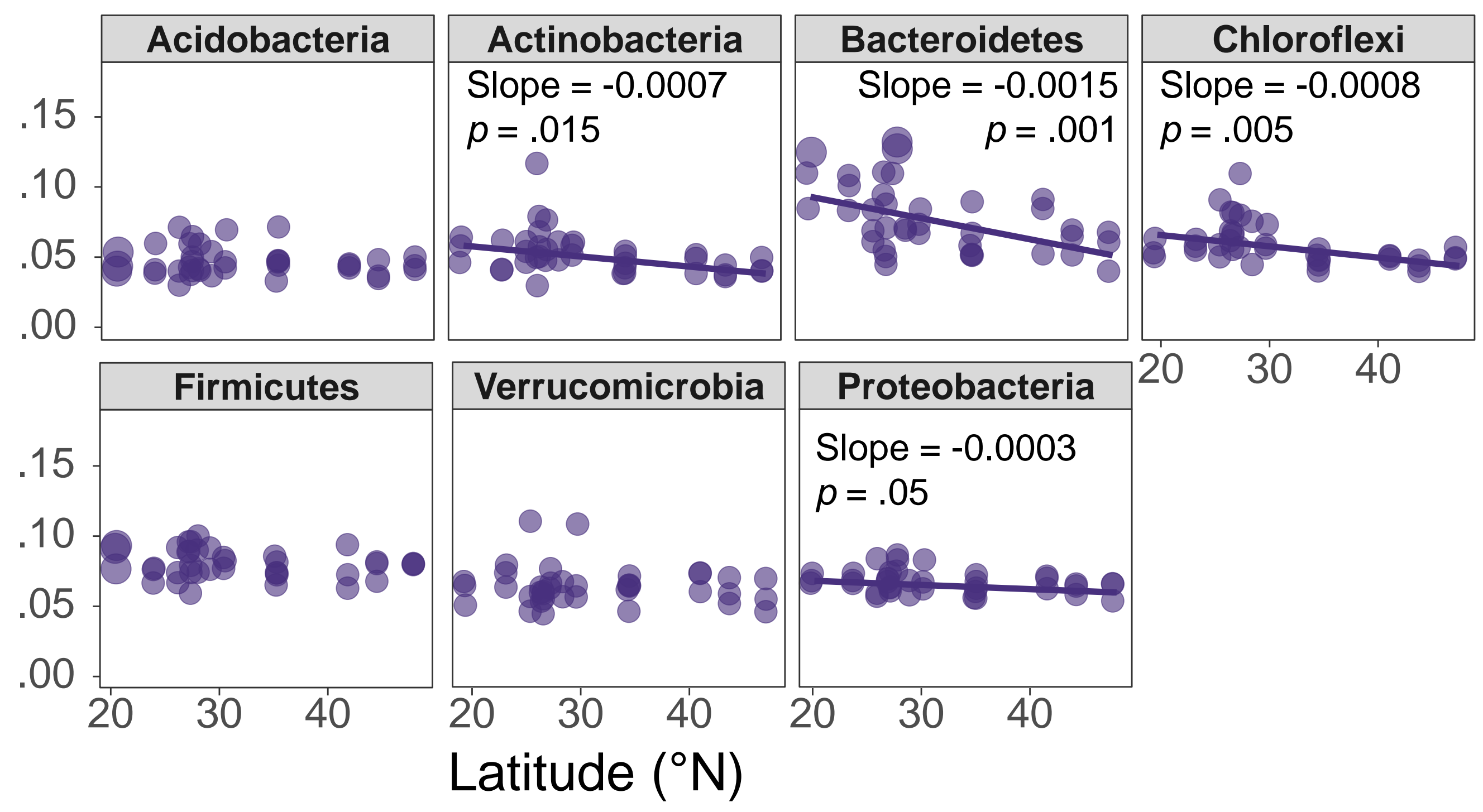


- HL (16.0°C)
- CC (17.8°C)
- SY (19.1°C)
- YY (22.8°C)
- FQ (24.3°C)
- LA (24.9°C)
- QZ (24.8°C)
- ZX (24.4°C)
- JO (25.9°C)
- CT (26.1°C)
- HY (24.8°C)
- QX (26.6°C)
- HK (27.8°C)

Functional genes

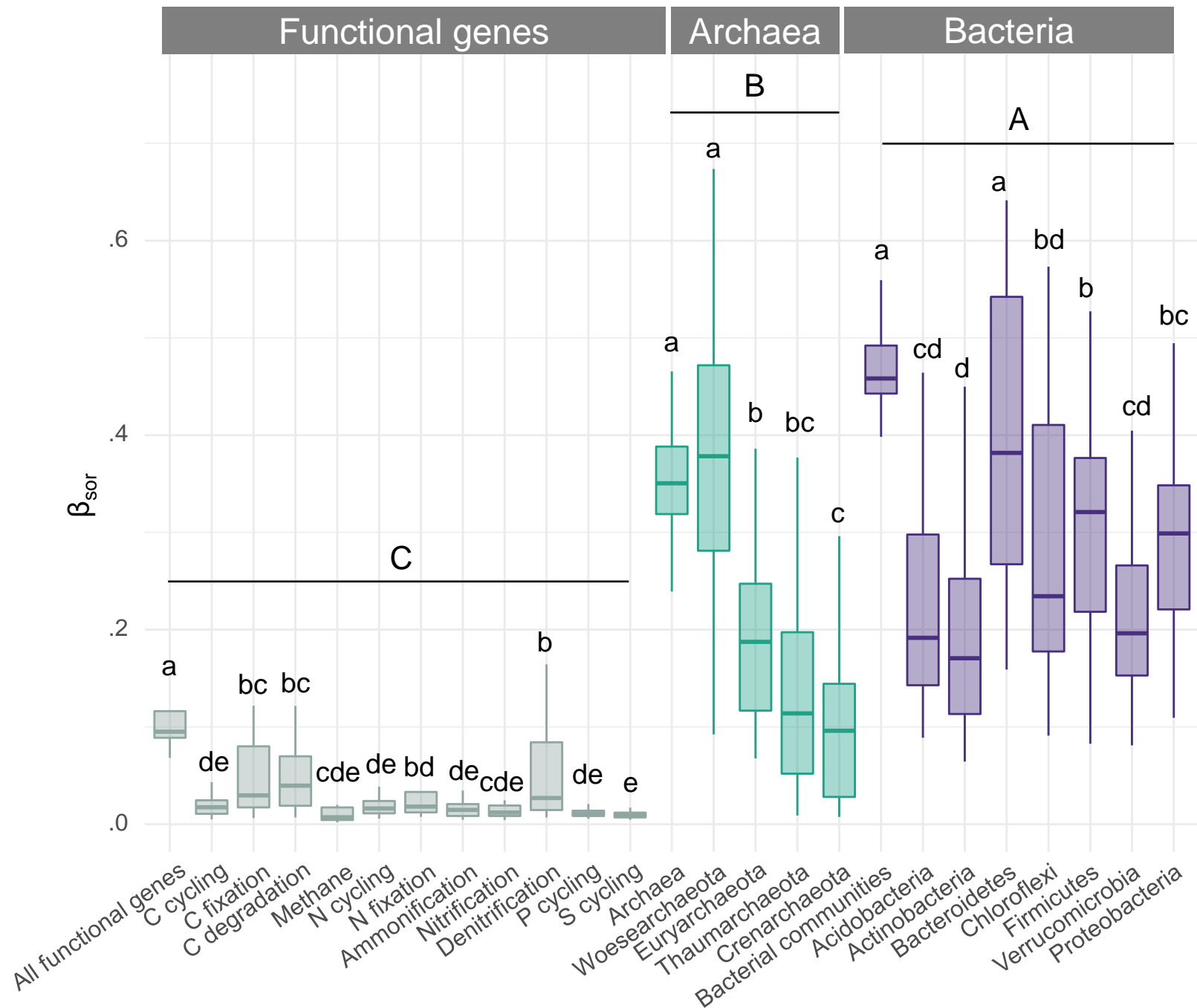


Archaea

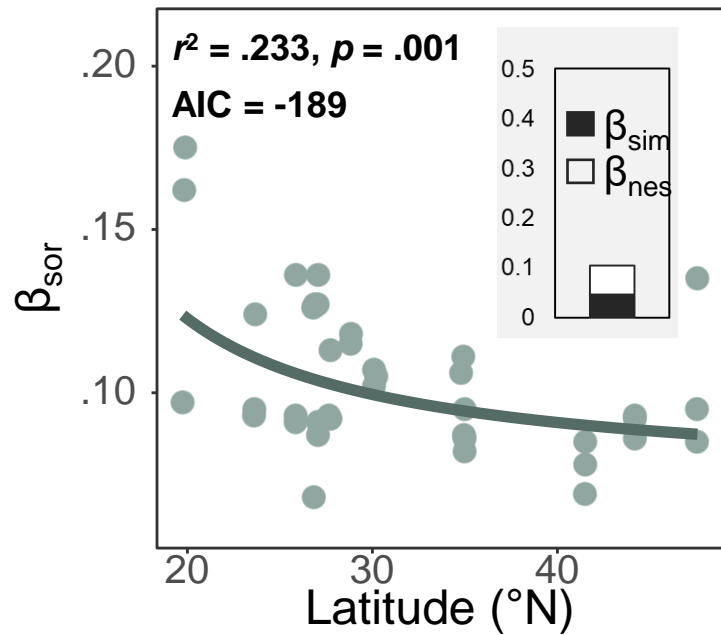


Bacteria

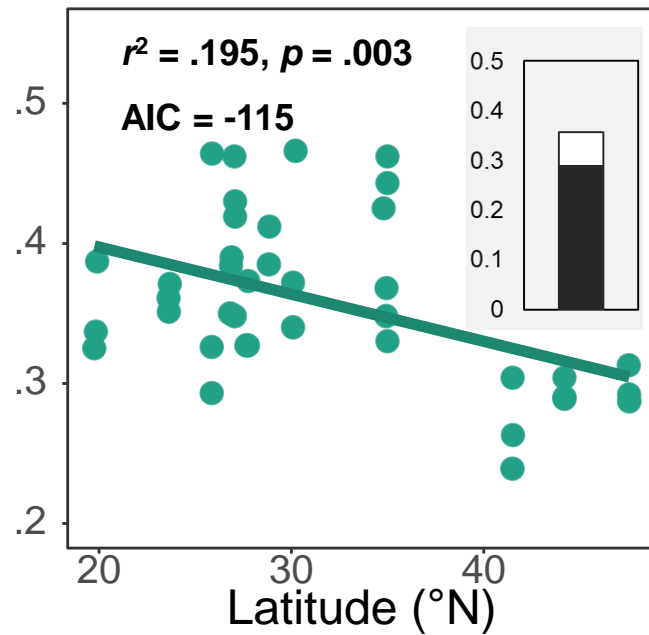
Latitude ($^{\circ}$ N)



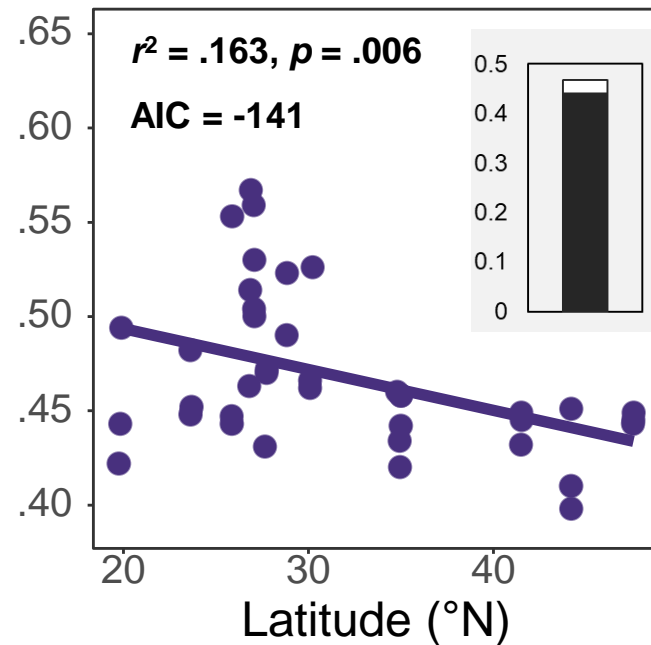
(a) Functional genes

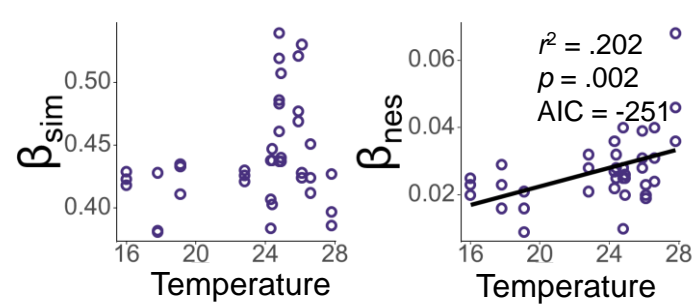
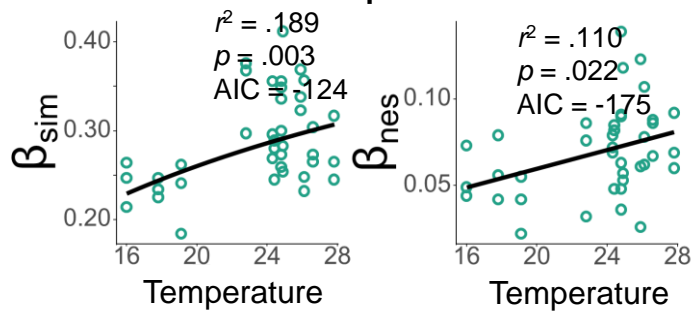
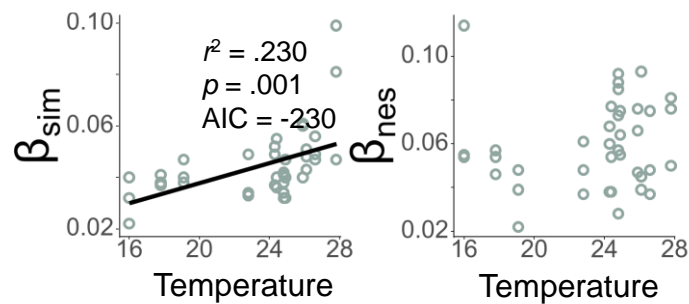
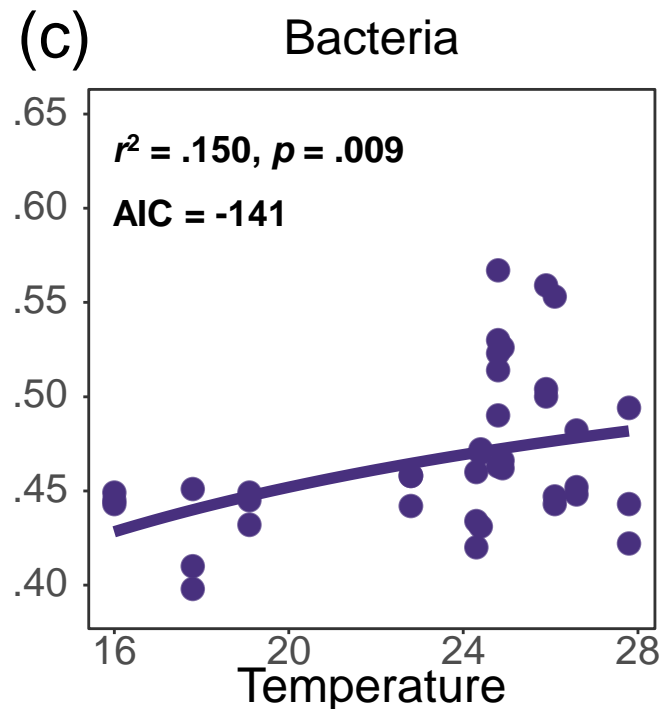
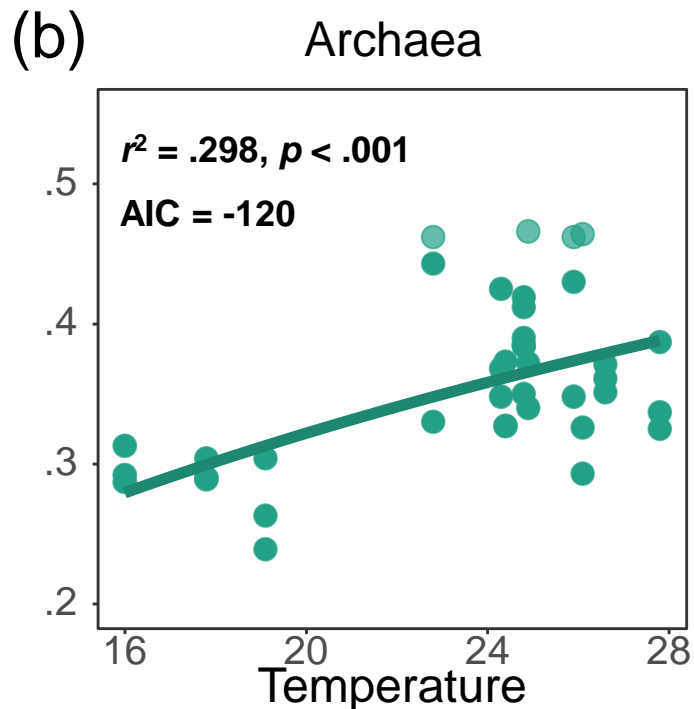
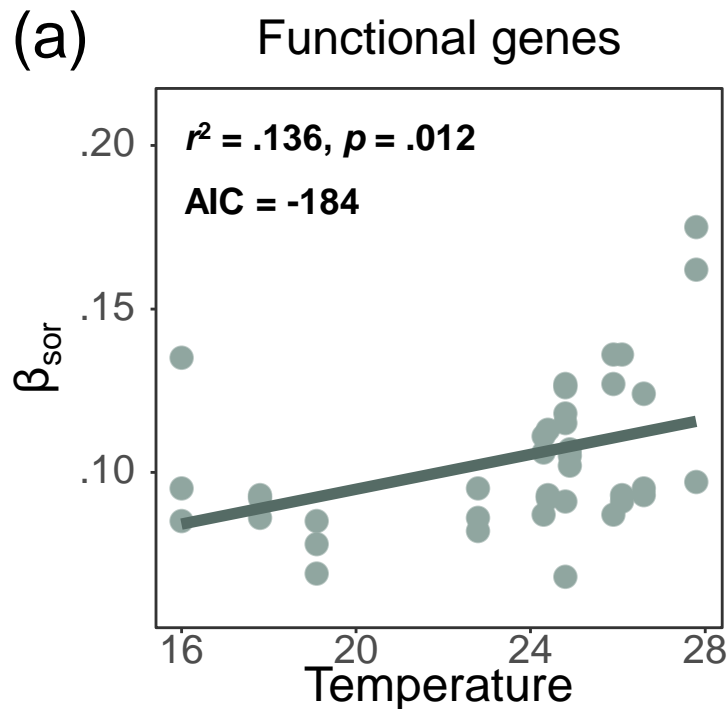


(b) Archaea



(c) Bacteria





SUPPORTING INFORMATION

Supplementary Materials: Methods and Results

Fig. S1 Taxa-area relationships for 39 paddy fields.

Fig. S2 The latitudinal patterns of β_z for different groups.

Fig. S3 The β_{sor} for different groups.

Fig. S4 The latitudinal patterns of β_{sor} .

Fig. S5 Relationships between temperature and β_{sor} .

Table S1 Information on the 39 paddy fields and the soil geochemical attributes.

Table S2 Summary of the TARs of both the power-law and semi-log model.

Table S3 The slopes of TARs in paddy fields.

Table S4 Summary of the curve estimations between latitude and temperature on β -diversity.

Table S5 Pearson correlation between β_{sor} and environmental conditions.

Table S6 VPA analysis of β_{sor} explained by temperature and soil heterogeneity.

Supplementary Materials

Methods

In each paddy field, the Sørensen dissimilarity index (β_{sor}) was calculated as the total β -diversity of microbial communities. Following Baselga (2010), we partitioned total β -diversity into two distinct parts: species turnover, measured by the Simpson dissimilarity index (β_{sim}), and the nestedness component (β_{nes}) derived by Baselga. The β_{sor} , β_{sim} , and β_{nes} are formulated as:

$$\beta_{sor} = \frac{b+c}{2a+b+c} \quad (1)$$

$$\beta_{sim} = \frac{\min(b,c)}{a+\min(b,c)} \quad (2)$$

$$\beta_{nes} = \beta_{sor} - \beta_{sim} = \frac{b+c}{2a+b+c} - \frac{\min(b,c)}{a+\min(b,c)} \quad (3)$$

where a is the number of genes or species present at both sites, b is the number of genes or species present at the first sampling point but not at the second, and c is the number of genes or species present at the second sampling point but not at the first. We calculated β -diversity metrics in R (version 3.5.1; <http://www.r-project.org/>) using the package ‘betapart’ (Baselga *et al.*, 2018). The mean total β -diversity and the relevant partition components were used for each latitude.

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Results

For comparison to assess the robustness of latitudinal patterns of soil microbial β -diversity, we also calculated the β -diversity of soil microbial communities and functional genes based on the Sørensen dissimilarity index (β_{sor}). Consistent with the results of β_z , the β_{sor} of microbial functional genes also showed the lowest values ($.104 \pm .023$), followed by the archaeal community ($.358 \pm .059$), and the soil bacterial community showed the highest β_{sor} values ($.468 \pm .041$) (Fig. S3). There was also considerable variation of β_{sor} within each group, with the highest being the functional genes involved in denitrification, Woese archaeota of archaeal community, and Bacteroidetes and Firmicutes of bacterial communities. The β_{sor} was then partitioned into species turnover (β_{sim}), which indicates species replacement, and nestedness (β_{nes}), which shows the species loss or gain (Fig. S4). The proportion of the species turnover in the total β -diversity was relatively lower than the nestedness component for the microbial functional genes ($\beta_{\text{sim}} = .045 \pm .014$, $\beta_{\text{nes}} = .059 \pm .020$). For archaeal and bacterial communities, the total β -diversity was attributed mainly to species turnover (archaea: $\beta_{\text{sim}} = .288 \pm .052$, $\beta_{\text{nes}} = .069 \pm .026$; bacteria: $\beta_{\text{sim}} = .441 \pm .041$, $\beta_{\text{nes}} = .027 \pm .010$).

The best-fit models between latitude and β_{sor} , with low AIC scores and high r^2 values, are presented in Fig. S4. For both soil microbial communities and functional genes, the total β -diversity

decreased significantly with latitude; the r^2 values were 0.233 ($p = .001$, AIC = -189), 0.195 ($p = .003$, AIC = -115), and 0.163 ($p = .006$, AIC = -141) for functional genes (inverse model), archaea (linear model), and bacteria (linear model), respectively.

The relationships between β -diversity and environmental factors, including geoclimate and soil geochemical heterogeneity, were further examined. Temperature during the growing season of rice plant was significantly and positively correlated with the β_{sor} of functional genes ($R = .399$, $p = .012$, AIC = -184) and archaeal ($R = .543$, $p < .001$, AIC = -119) and bacterial ($R = .413$, $p = .009$, AIC = -141) communities by Pearson correlation analysis (Table S5). The variation partitioning analysis also suggested the more important role of temperature (16.46 – 21.13%) in driving microbial β -diversity than soil heterogeneity (0.88 – 11.84%) (Table S6). Linear, exponential, and inverse models were further used to fit the best models between the temperature during the growing season and β_{sor} (Table S4). The results indicated that β_{sor} increased significantly with temperature; the r^2 values were .136 ($p = .012$, AIC = -184), .298 ($p < .001$, AIC = -120), and .150 ($p = .009$, AIC = -141) for functional genes (linear model), archaea (inverse model), and bacteria (inverse model), respectively (Fig. S5). To partition the total β -diversity into species turnover (β_{sim}) and nestedness (β_{nes}), we found that the β_{sim} of functional genes and archaea, and the β_{nes} of archaea and bacteria also increased significantly with temperature.

Supplementary Figures

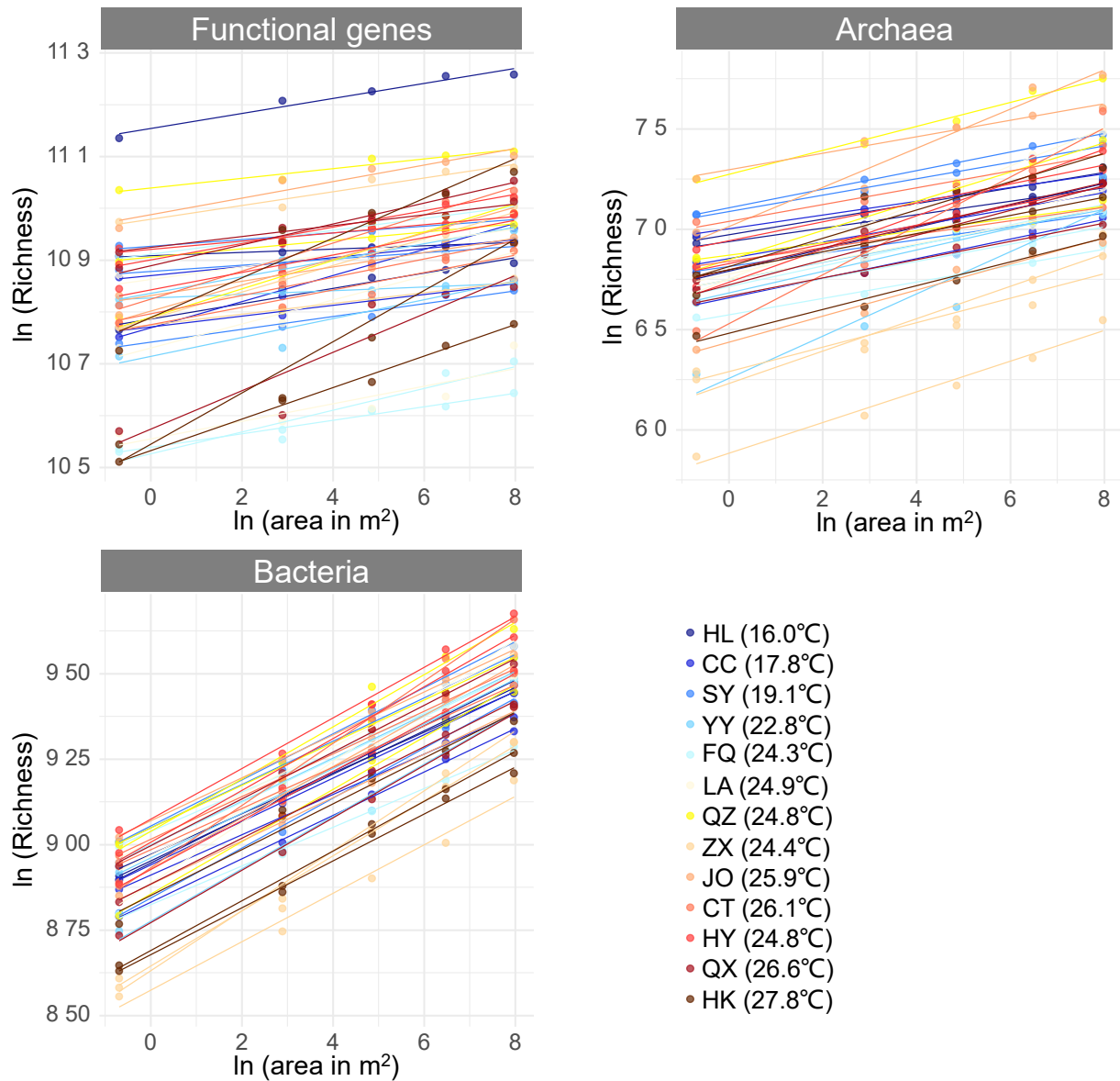


Fig. S1 Taxa-area relationships for 39 paddy fields spanning a wide temperature and latitudinal gradient in China. Mean temperature during the growing season of the rice plants at each site are marked in the legend.

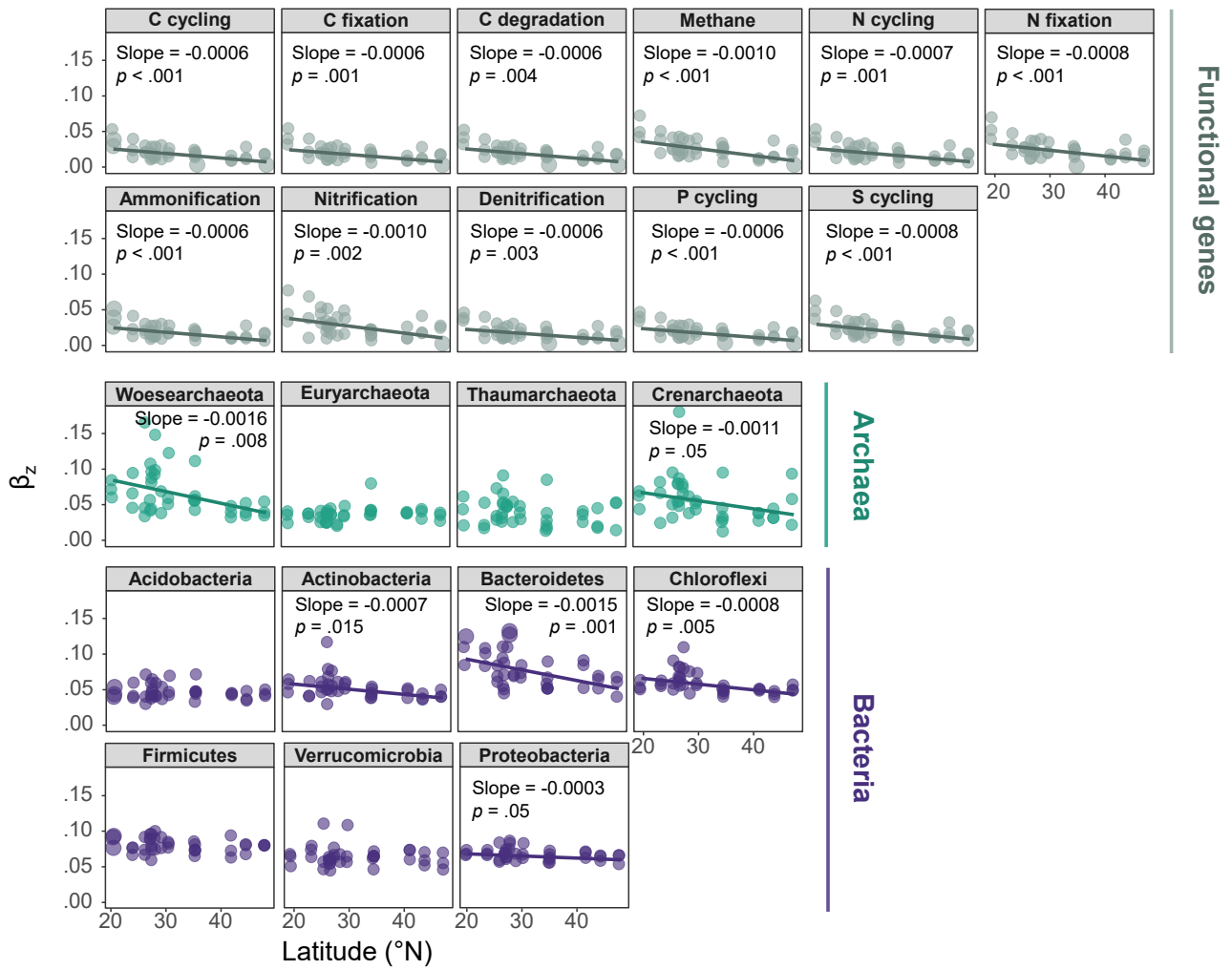


Fig. S2 The latitudinal patterns of β -diversity (β_z) for different taxonomic groups and subgroups of functional genes.

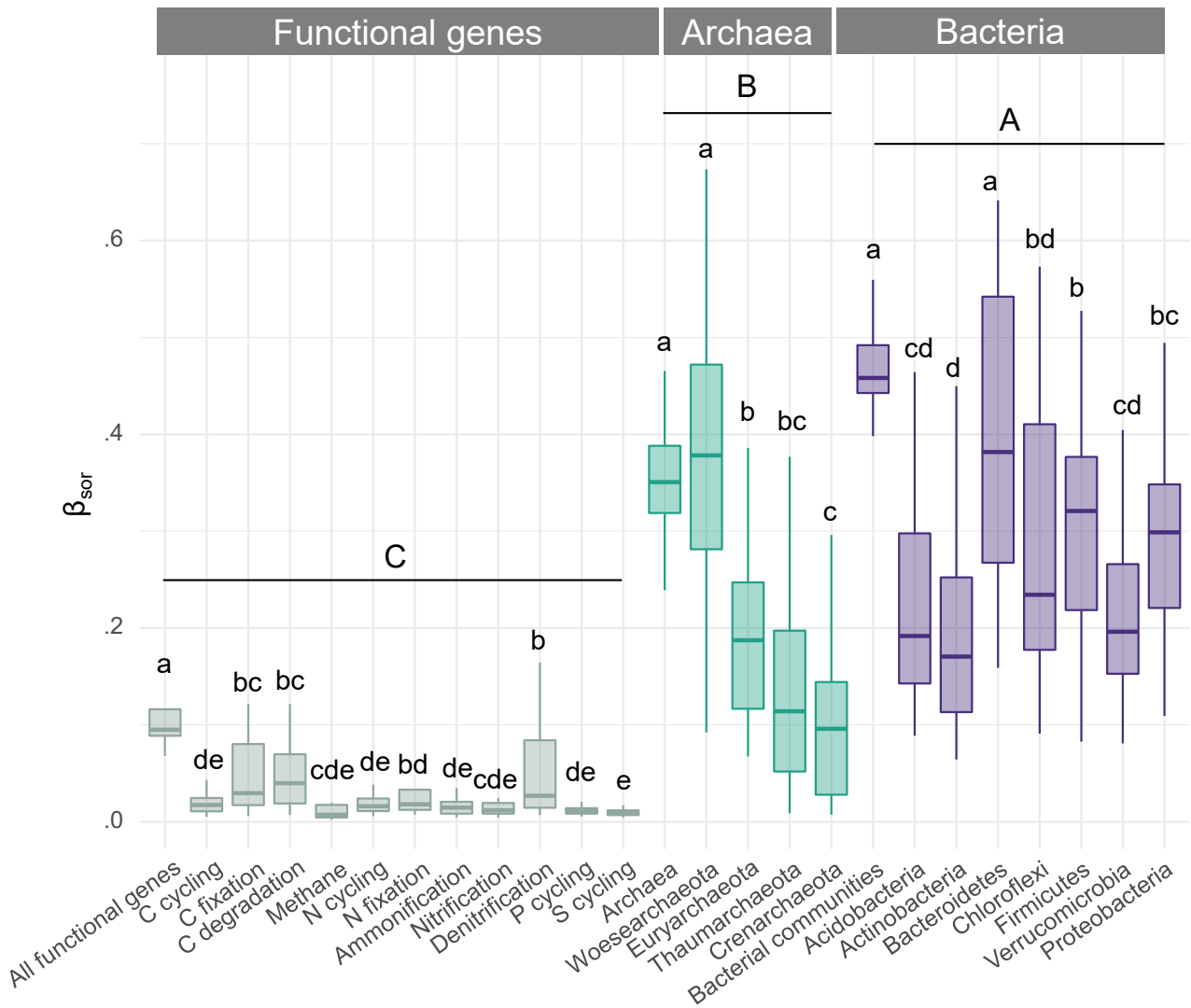


Fig. S3 The β -diversity (β_{sor}) for different taxonomic groups and subgroups of functional genes. Uppercase letters indicate significant differences (Duncan's multiple-range test at $p < 0.05$) between the functional genes, archaea, and bacteria; lowercase letters indicate significant differences between subgroups.

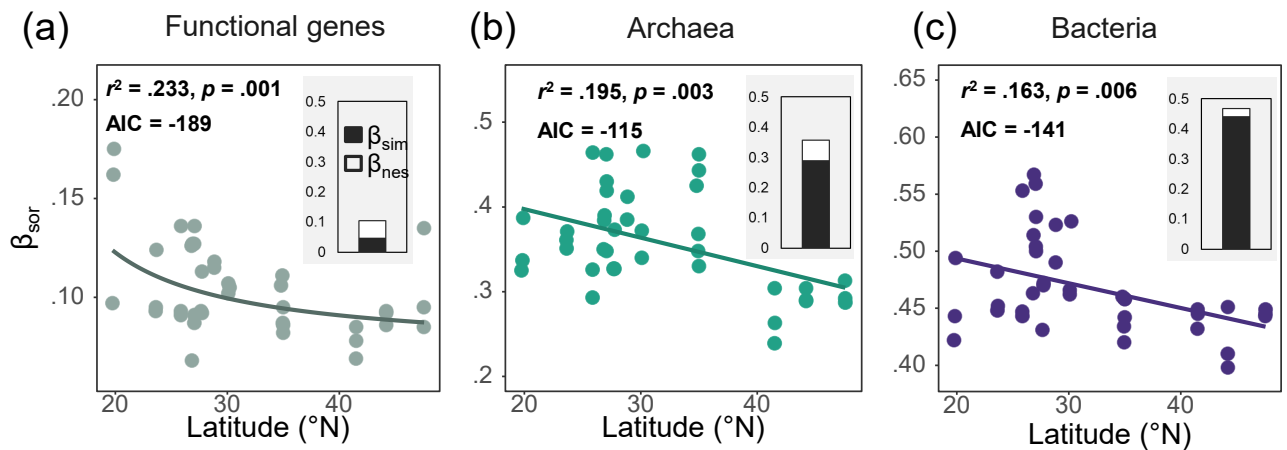


Fig. S4 The latitudinal patterns of microbial β -diversity based on the Sørensen dissimilarity index (β_{sor}). The inserts in (b) are two distinct components of total β -diversity, including β_{sim} and β_{nes} . Linear, exponential, and inverse models were used to estimate the relationships between latitude and β -diversity indices, and the best-fit models with low Akaike's information criterion (AIC) scores and high r^2 values are presented.

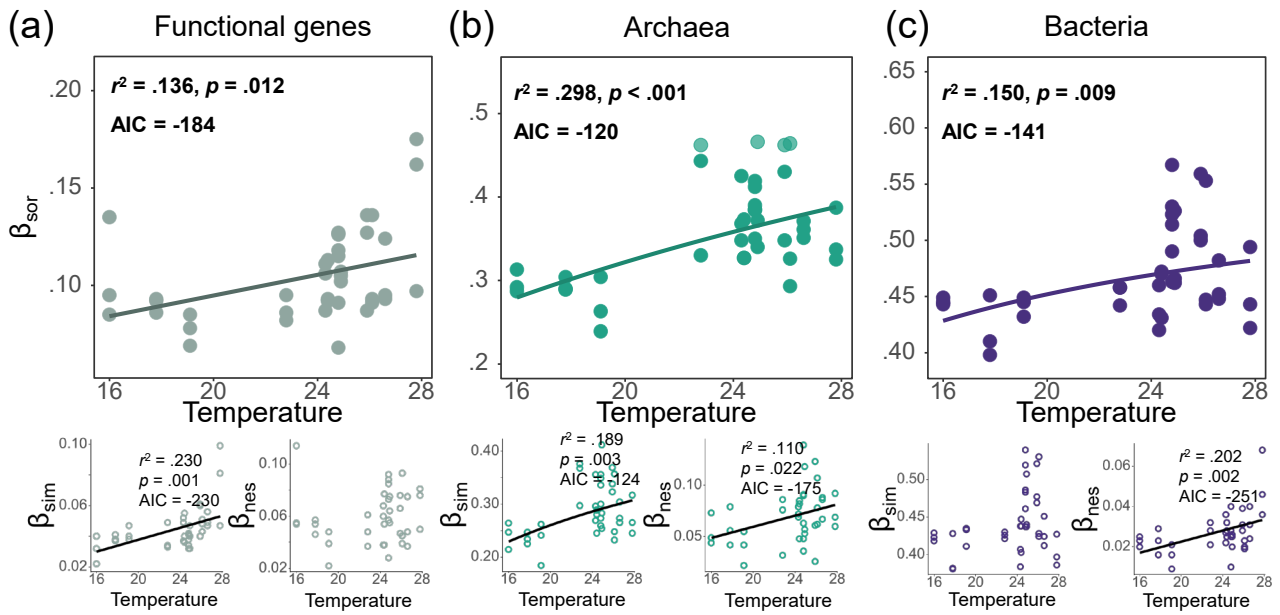


Fig. S5 Relationships between temperature during the growing season of rice plants and microbial β -diversity based on the Sørensen dissimilarity index (β_{sor}), as well as two distinct components (β_{sim} and β_{nes}). Temperature refers to the mean temperature during the growing season of rice plant. Linear, exponential, and inverse models were used to estimate the relationships between environmental temperature and β -diversity, and the best-fit models with low Akaike's information criterion (AIC) scores and high r^2 values are presented.

Supplementary Tables

Table S1 Information on the 39 paddy fields and the average soil geochemical attributes of 11 samples at each site.

Mean temperature during the growing season	Annual temperature difference	Precipitation during the growing season	Soil type	Rice cultivation and yield			Plot	Coordinates	NO ₃ ⁻ -N	NH ₄ ⁺ -N	TN	OM	pH	Soil texture		
				N rate (kg N/ha)	P rate (kg P/ha)	Yield (Mg/ha)			(mg/kg)	(mg/kg)	(g/kg)	(g/kg)		Clay (%)	Silt (%)	Sand (%)
16.0	15.9	614	Neutral black soil derived from loamy loess	362.45	95.19	7.08	HLa	47.579°N, 126.884°E	0.55 (103%)*	8.60 (19%)	3.04 (11%)	58.32 (7%)	5.87 (3%)	24.90	67.46	7.64
							HLb	47.566°N, 126.892°E	2.07 (108%)	4.84 (16%)	3.20 (9%)	66.10 (6%)	5.84 (3%)	22.40	66.39	11.21
							HLc	47.554°N, 126.929°E	1.61 (45%)	5.04 (13%)	2.77 (8%)	64.05 (5%)	6.57 (5%)	51.80	48.20	0.00
17.8	14	566	Neutral black soil derived from loamy loess	473.18	46.89	7.59	CCa	44.207°N, 125.572°E	5.22 (27%)	4.96 (16%)	2.49 (13%)	45.60 (6%)	7.59 (3%)	17.00	65.77	17.23
							CCb	44.205°N, 125.576°E	6.71 (25%)	4.70 (17%)	2.32 (10%)	40.10 (11%)	7.97 (5%)	20.40	66.14	13.46
							CCc	44.207°N, 125.569°E	7.22 (15%)	4.78 (12%)	2.65 (21%)	39.15 (6%)	8.02 (2%)	15.20	68.72	16.08
19.1	12.9	652	Neutral black soil derived from loamy loess	497.73	86.86	8.50	SYa	41.516°N, 123.353°E	1.96 (140%)	5.45 (10%)	1.35 (14%)	25.11 (10%)	7.62 (4%)	13.90	65.48	20.62
							SYb	41.525°N, 123.322°E	1.18 (127%)	5.36 (30%)	1.31 (10%)	22.69 (4%)	7.17 (1%)	16.50	63.10	20.40
							SYc	41.502°N, 123.324°E	0.71 (164%)	5.23 (15%)	1.56 (9%)	30.00 (5%)	6.49 (4%)	21.30	62.26	16.44

22.8	10	416	Alkaline fluvo-aquic soil derived from alluvial sediments of the Yellow River	471.57	233.77	7.56	YYa	35.003°N, 114.129°E	23.75 (29%)	1.71 (18%)	0.98 (38%)	13.81 (40%)	8.41 (1%)	9.50	61.86	28.64
							YYb	35.001°N, 114.052°E	27.89 (48%)	2.69 (18%)	1.13 (21%)	16.70 (21%)	8.45 (2%)	7.90	67.15	24.95
							YYc	35.003°N, 114.089°E	27.19 (32%)	1.86 (12%)	1.44 (16%)	23.84 (20%)	8.43 (2%)	11.80	71.73	16.47
24.3	10	428	Alkaline fluvo-aquic soil derived from alluvial sediments of the Yellow River	490.06	243.81	6.60	FQa	34.958°N, 114.574°E	26.25 (19%)	1.57 (29%)	1.42 (21%)	23.29 (11%)	8.31 (2%)	13.60	58.85	27.55
							FQb	34.804°N, 114.457°E	31.61 (24%)	1.66 (16%)	1.54 (20%)	28.38 (8%)	8.44 (1%)	10.10	71.05	18.85
							FQc	34.933°N, 114.573°E	24.39 (39%)	1.45 (38%)	0.89 (42%)	13.11 (45%)	8.40 (1%)	6.70	42.30	51.00
24.9	8.8	924	Hydromorphic paddy soils derived from sediments of lakes	382.80	86.60	7.29	LAa	30.230°N, 119.796°E	20.57 (40%)	4.43 (22%)	0.36 (79%)	2.81 (15%)	7.10 (9%)	18.70	74.32	6.98
							LAb	30.097°N, 119.766°E	8.67 (99%)	12.44 (27%)	1.02 (17%)	2.95 (32%)	4.93 (4%)	21.80	61.25	16.95
							LAc	30.084°N, 119.732°E	36.18 (23%)	6.35 (10%)	1.23 (34%)	3.49 (4%)	5.01 (4%)	16.20	69.35	14.45
24.8	8.5	1078	Hydromorphic paddy soils derived from sediments of lakes	358.13	81.26	6.78	QZa	28.834°N, 118.869°E	3.53 (42%)	29.60 (38%)	2.46 (17%)	4.34 (15%)	4.53 (2%)	22.30	64.74	12.96
							QZb	27.083°N, 118.432°E	3.97 (159%)	9.78 (17%)	2.58 (9%)	4.88 (9%)	4.71 (2%)	19.00	64.24	16.76
							QZc	28.855°N, 119.014°E	3.63 (101%)	17.17 (32%)	2.06 (10%)	4.14 (5%)	5.53 (17%)	24.40	70.13	5.47
24.4	6.7	1220	Acidic red soil derived from Quaternary red clay	213.98	110.87	1.73	ZXa	27.661°N, 117.012°E	10.85 (49%)	5.06 (29%)	1.15 (37%)	16.86 (23%)	5.11 (4%)	12.50	21.03	66.47
							ZXb	27.755°N, 116.995°E	23.13 (59%)	9.39 (144%)	1.61 (29%)	27.47 (23%)	4.99 (3%)	7.30	5.76	86.94

							ZXc	27.742°N, 116.976°E	30.64 (25%)	5.46 (23%)	1.56 (23%)	31.93 (21%)	4.83 (2%)	8.00	32.06	59.94
25.9	6.9	845	Acidic red soil derived from Quaternary red clay	417.74	149.38	6.07	JOa	27.067°N, 118.367°E	27.98 (45%)	3.17 (21%)	0.86 (10%)	2.48 (8%)	5.82 (4%)	23.90	61.39	14.71
							JOb	27.050°N, 118.303°E	3.70 (168%)	7.69 (56%)	1.04 (26%)	3.28 (17%)	4.07 (20%)	15.30	13.59	71.11
							JOc	27.083°N, 118.432°E	0.62 (101%)	5.98 (29%)	1.75 (24%)	4.43 (31%)	4.86 (4%)	20.10	75.41	4.49
26.1	5.9	804	Acidic red soil derived from Quaternary red clay	487.20	174.30	6.08	CTa	25.861°N, 116.176°E	31.54 (45%)	7.00 (31%)	1.78 (9%)	3.66 (8%)	4.88 (17%)	10.30	46.46	43.24
							CTb	25.882°N, 116.142°E	24.92 (81%)	5.27 (50%)	1.67 (34%)	3.06 (36%)	6.58 (37%)	16.40	74.58	9.02
							CTc	25.866°N, 116.183°E	3.50 (226%)	11.68 (18%)	1.84 (8%)	3.58 (9%)	5.13 (3%)	15.30	56.43	28.27
24.8	8.7	777	Acidic red soil derived from Quaternary red clay	355.80	90.56	6.34	HYa	26.856°N, 113.019°E	16.13 (26%)	5.39 (16%)	1.60 (9%)	3.40 (7%)	4.93 (13%)	21.50	78.50	0.00
							HYb	26.898°N, 113.054°E	16.66 (107%)	7.25 (33%)	1.69 (16%)	3.36 (16%)	4.77 (6%)	51.60	48.40	0.00
							HYc	26.813°N, 113.016°E	28.48 (59%)	8.56 (83%)	1.93 (28%)	3.37 (12%)	4.63 (5%)	18.00	71.53	10.47
26.6	5.6	1030	Submergienc paddy soil derived from neritic sediment	567.70	123.66	5.72	QXa	23.634°N, 112.842°E	7.85 (53%)	3.17 (30%)	1.58 (19%)	24.54 (8%)	6.61 (10%)	19.80	61.53	18.67
							QXb	23.618°N, 112.813°E	4.62 (79%)	3.76 (10%)	1.49 (22%)	20.93 (12%)	5.61 (5%)	12.90	59.77	27.33
							QXc	23.685°N, 112.930°E	0.95 (116%)	4.64 (15%)	1.94 (25%)	34.39 (13%)	6.30 (7%)	20.70	63.08	16.22
27.8	4.2	1704	Submergienc paddy soil derived	550.19	131.42	4.73	HKa	19.897°N, 110.425°E	0.40 (73%)	4.64 (18%)	1.24 (19%)	19.61 (11%)	5.43 (4%)	17.70	65.23	17.07

	from marine sediment	HKb	19.841°N, 110.417°E	24.92 (61%)	23.66 (63%)	1.45 (13%)	21.89 (9%)	5.00 (3%)	19.70	61.01	19.29
		HKc	19.758°N, 110.512°E	1.78 (170%)	16.78 (95%)	2.01 (32%)	29.78 (11%)	5.59 (3%)	21.60	69.03	9.37

*Numbers in the brackets indicate coefficient of variation (CV) of soil geochemical variables within each plot. TN = total nitrogen; OM = organic matter; NPP = net primary productivity.

Table S2 Summary of the TARs of both the power-law and semi-log model for the functional genes in paddy fields from North to South China.

Sites	Power-law			Semi-log model		
	r^2	p	AIC	r^2	p	AIC
HLa	.947	.003	-27.00	.953	.003	84.37
HLb	.969	.001	-44.91	.969	.002	64.42
HLc	.936	.004	-25.82	.945	.004	81.66
CCa	.955	.003	-31.20	.950	.003	77.57
CCb	.968	.002	-24.14	.969	.001	84.24
CCc	.926	.006	-30.40	.925	.006	78.65
SYa	.928	.005	-33.50	.923	.006	76.37
SYb	.866	.014	-30.81	.859	.015	78.51
SYc	.941	.004	-28.09	.935	.005	80.36
YYa	.938	.004	-25.25	.948	.003	82.72
YYb	.840	.018	-18.77	.840	.018	89.06
YYc	.973	.001	-44.68	.930	.001	63.80
FQa	.977	.001	-32.41	.976	.001	73.60
FQb	.850	.017	-17.72	.840	.018	88.82
FQc	.976	.001	-33.47	.971	.001	77.06
LAA	.885	.011	-18.20	.869	.013	90.75
LAb	.679	.050	-15.30	.651	.060	91.68
LAc	.760	.030	-20.45	.747	.037	89.11
QZa	.758	.003	-12.29	.759	.035	96.61
QZb	.913	.007	-28.83	.912	.007	81.93
QZc	.963	.002	-34.67	.965	.002	74.30
ZXa	.975	.001	-34.30	.970	.001	74.79
ZXb	.971	.001	-24.50	.962	.002	85.79
ZXc	.924	.006	-26.04	.923	.006	84.30
JOa	.900	.009	-22.72	.912	.007	86.96
JOb	.944	.004	-21.27	.928	.005	89.08
JOc	.908	.008	-24.61	.900	.009	84.73
CTa	.874	.013	-20.98	.863	.014	87.97
CTb	.975	.001	-29.03	.981	.001	78.27
CTc	.977	.001	-25.03	.973	.001	85.03
HYa	.973	.001	-29.58	.972	.001	80.07
HYb	.893	.010	-29.30	.890	.010	80.40
HYc	.926	.006	-23.81	.916	.007	86.02
QXa	.963	.002	-32.07	.962	.002	77.70
QXb	.967	.002	-26.16	.959	.002	84.65
QXc	.734	.018	-8.04	.674	.028	122.88
HKa	.901	.009	-11.45	.873	.013	97.37
HKc	.989	< .001	-27.81	.985	< .001	80.36

Table S3 The slopes (β_z) of the taxa-area relationships for the functional genes, archaea, and bacteria in paddy fields from North to South China.

Sites	Functional genes				Archaea				Bacteria			
	β_z	$\ln c^*$	r^2	p	β_z	$\ln c$	r^2	p	β_z	$\ln c$	r^2	p
HLa	.015	11.15	.947	.003	.039	6.97	.979	.001	.063	8.95	.999	<.001
HLb	.003	10.91	.969	.001	.055	6.79	.973	.002	.060	8.97	.999	<.001
HLc	.015	10.79	.936	.005	.034	6.94	.978	.001	.067	8.95	.999	<.001
CCa	.011	10.77	.955	.003	.034	7.00	.989	<.001	.064	8.94	.999	<.001
CCb	.025	10.77	.968	.002	.049	6.66	.989	<.001	.064	8.83	.999	<.001
CCc	.009	10.87	.926	.006	.041	6.85	.993	<.001	.059	8.91	.998	<.001
SYa	.006	10.93	.928	.005	.046	7.11	.999	<.001	.067	9.05	.998	<.001
SYb	.006	10.88	.865	.014	.041	7.09	.990	<.001	.063	9.05	.997	<.001
SYc	.012	10.74	.941	.004	.033	6.81	.987	.001	.073	8.84	.996	.001
YYa	.016	10.84	.938	.004	.044	7.75	.976	.002	.063	9.00	.995	<.001
YYb	.018	10.71	.840	.018	.054	6.68	.992	<.001	.065	8.96	.997	<.001
YYc	.004	10.83	.973	.001	.105	6.26	.883	.018	.077	8.78	.985	.004
FQa	.013	10.54	.977	<.001	.041	6.57	.986	.001	.069	8.82	.996	.001
FQb	.021	10.53	.850	.017	.043	6.67	.992	<.001	.064	9.04	.998	<.001
FQc	.012	10.91	.976	.001	.051	6.71	.977	.001	.063	9.00	.992	<.001
LAA	.023	10.73	.885	.011	.094	6.75	.998	<.001	.089	8.89	.980	.003
LAB	.017	10.56	.679	.050	.045	6.75	.924	.009	.065	8.97	.997	.001
LAC	.012	10.86	.760	.034	.052	6.78	.982	.001	.069	9.01	.998	<.001
QZa	.027	10.79	.758	.035	.060	7.27	.986	.001	.077	8.86	.997	<.001
QZb	.009	11.04	.913	.007	.073	6.85	.942	.006	.076	9.04	.968	.003
QZc	.008	10.91	.962	.002	.031	6.87	.957	.004	.062	9.05	.999	<.001
ZXa	.010	10.78	.975	.001	.077	5.88	.975	.002	.071	8.57	.977	.007
ZXb	.026	10.79	.971	.001	.081	6.23	.907	.012	.081	8.65	.994	.002

ZXc	.013	10.98	.923	.006	.061	6.29	.912	.011	.088	8.63	.964	.004
JOa	.016	10.99	.900	.009	.065	6.44	.976	.002	.063	9.07	.997	<.001
JOb	.025	10.80	.944	.004	.041	7.30	.981	.001	.064	8.88	.997	.001
JOc	.014	10.83	.908	.008	.098	7.01	.967	.003	.075	8.93	.993	.001
CTa	.017	10.78	.874	.013	.034	6.84	1.000	<.001	.062	9.02	.997	<.001
CTb	.018	10.80	.975	.001	.122	6.53	.972	.002	.091	8.93	.994	.002
CTc	.027	10.82	.977	<.001	.042	7.04	.951	.005	.060	8.99	.999	<.001
HYa	.016	10.90	.973	.001	.047	6.94	.987	.001	.076	9.01	.980	.002
HYb	.008	10.92	.893	.010	.083	6.74	.960	.003	.074	9.07	.993	.002
HYc	.017	10.84	.926	.006	.048	6.83	.991	<.001	.072	8.93	.999	.001
QXa	.011	10.92	.963	.002	.045	6.67	.992	<.001	.067	8.88	.999	<.001
QXb	.020	10.89	.967	.002	.054	6.80	.989	.001	.068	9.00	.997	<.001
QXc	.037	10.57	.795	.027	.062	6.72	.992	<.001	.077	8.77	.996	.002
HKa	.050	10.55	.901	.009	.045	6.80	.998	<.001	.073	8.69	.997	.001
HKb	.038	10.79	.895	.010	.071	6.81	.862	.023	.067	8.85	.974	<.001
HKc	.030	10.53	.989	<.001	.059	6.48	.977	.001	.069	8.68	.995	<.001

* $\ln c$ is the intercept of the log-linear model of taxa-area relationships.

Table S4 Summary of the curve estimations, including linear, exponential, and inverse models, for the potential effects of latitude and mean temperature during the growing season of rice plant on β -diversity indices of the functional genes, archaea, and bacteria in paddy fields.

		β_{sor}			β_{sim}			β_{nes}			β_z			
		Functional genes	Archaea	Bacteria	Functional genes	Archaea	Bacteria	Functional genes	Archaea	Bacteria	Functional genes	Archaea	Bacteria	
Latitude	Linear model	r^2	.18	.19	.16	.24	.10	.07	.02	.10	.22	.28	.16	.15
		p	.006	.003	.006	.001	.029	.055	.405	.028	.002	.001	.029	.017
		AIC	-185	-115	-141	-231	-120	-138	-191	-174	-252	-257	-189	-263
	Exponential model	r^2	.16	.23	.17	.27	.12	.07	.00	.10	.19	.28	.16	.16
		p	.007	.001	.005	< .001	.016	.056	.329	.028	.003	< .001	.013	.024
		AIC	-13	-36	-85	0	-24	-76	32	40	29	-260	-188	-263
	Inverse model	r^2	.23	.10	.09	.35	.03	.01	.00	.08	.31	.39	.09	.11
		p	.001	.030	.034	< .001	.148	.228	.318	.050	< .001	< .001	.069	.040
		AIC	-189	-110	-138	-237	-117	-135	-191	-173	-257	-264	-188	-262
Temperature during the growing season	Linear model	r^2	.14	.28	.15	.23	.16	.06	.01	.11	.20	.22	.09	.07
		p	.012	< .001	.009	.001	.006	.066	.504	.022	.002	.001	.034	.056
		AIC	-184	-119	-141	-230	-123	-137	-190	-175	-251	-255	-189	-261
	Exponential model	r^2	.14	.32	.16	.27	.19	.06	.01	.11	.19	.25	.12	.07
		p	.011	< .001	.008	< .001	.003	.067	.380	.023	.003	.001	.017	.052
		AIC	-13	-40	-84	-1	-28	-76	33	40	29	63	26	-55
	Inverse model	r^2	.09	.30	.15	.18	.19	.07	.02	.10	.15	.16	.10	.08
		p	.037	< .001	.009	.004	.003	.053	.676	.027	.008	.006	.031	.048
		AIC	-182	-120	-141	-228	-124	-138	-190	-174	-249	-253	-189	-261

The best fit models with lower Akaike's information criterion (AIC) and higher r^2 were marked in bold.

Table S5 Pearson correlation between β -diversity (β_{sor}) of the soil functional genes and microbial communities and environmental conditions.

	Functional genes			Archaea			Bacteria		
	R	<i>p</i>	AIC	R	<i>p</i>	AIC	R	<i>p</i>	AIC
Temperature	.399	.012	-184	.543	< .001	-119	.413	.009	-141
Precipitation	.496	.001	-188	.065	.694	-105	.184	.261	-135
Soil heterogeneity									
pH	.004	.292	-178	.127	.015	-112	.197	.003	-143
OM	-.021	.642	-177	-.014	.497	-106	.081	.044	-138
NH ₄ ⁺ -N	.062	.069	-181	-.026	.876	-105	-.016	.526	-134
NO ₃ ⁻ -N	.057	.078	-180	.033	.138	-108	.057	.078	-137
TN	-.006	.381	-178	-.026	.856	-105	.056	.079	-137
C/N	-.026	.819	-177	-.008	.414	-106	.044	.107	-136

Temperature and precipitation refer to the mean temperature and accumulated precipitation during the growing season of rice plant, respectively; OM = organic matter; TN = total nitrogen. The heterogeneity of soil was indicated by the variance of each soil variable (pH, OM, NH₄⁺-N, NO₃⁻-N, TN, and C/N) within a site. *p* < .05 indicates significant correlations and is listed in bold font.

Table S6 Variation partitioning analysis of microbial β -diversity (β_{sor}) explained by mean temperature during the growing season of rice plant and soil heterogeneity.

	Temperature (%)	Soil heterogeneity (%)	Shared (%)	Unexplained (%)
Functional genes	16.46	0.88	1.94	80.72
Archaea	21.13	2.89	7.80	68.18
Bacteria	19.48	11.84	1.34	67.34

Temperature refers to the mean temperature during the growing season of rice plant.